SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 18:03:10 ; Search time 3255 Seconds
                                              (without alignments)
                                              5165.547 Million cell updates/sec

Title: US-10-036-959B-8
Perfect score: 2057
Sequence: 1 MSPSSDSINPRDVCIVGVAR.........GASALVLELMSVGRVGRSLL 411

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop   6.0 , Delext   7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US10036959/runat_04122003_161437_22952/app_query.fasta_1.5
83
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10036959_@CGN_1_1_2372_@runat_04122003_161437_22952 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
                1: gb_ba:*
                2: gb_htg:*
                3: gb_in:*
                4: gb_om:*
                5: gb_ov:*
                6: gb_pat:*
                7: gb_ph:*
                8: gb_pl:*
                9: gb_pr:*
                10: gb_ro:*

```
11:    gb_sts:*
12:    gb_sy:*
13:    gb_un:*
14:    gb_vi:*
15:    em_ba:*
16:    em_fun:*
17:    em_hum:*
18:    em_in:*
19:    em_mu:*
20:    em_om:*
21:    em_or:*
22:    em_ov:*
23:    em_pat:*
24:    em_ph:*
25:    em_pl:*
26:    em_ro:*
27:    em_sts:*
28:    em_un:*
29:    em_vi:*
30:    em_htg_hum:*
31:    em_htg_inv:*
32:    em_htg_other:*
33:    em_htg_mus:*
34:    em_htg_pln:*
35:    em_htg_rod:*
36:    em_htg_mam:*
37:    em_htg_vrt:*
38:    em_sy:*
39:    em_htgo_hum:*
40:    em_htgo_mus:*
41:    em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2057	100.0	1669	8	AF429383	AF429383 Hevea bra
2	1701	82.7	1444	8	AY088740	AY088740 Arabidops
3	1670	81.2	1736	8	AF364059	AF364059 Arabidops
4	1661	80.7	1492	8	AF411795	AF411795 Arabidops
5	1637	79.6	1228	8	AY091271	AY091271 Arabidops
6	1637	79.6	1531	8	AY059736	AY059736 Arabidops
7	1579.5	76.8	1462	6	AR242842	AR242842 Sequence
8	1579.5	76.8	1462	6	AX105331	AX105331 Sequence
9	1579.5	76.8	1462	6	AX105578	AX105578 Sequence
10	1579.5	76.8	1462	8	RSLAACT	X78116 R.sativus L
11	1300.5	63.2	82503	8	AB016886	AB016886 Arabidops
c 12	1247.5	60.6	59372	8	AB023039	AB023039 Arabidops
c 13	1154.5	56.1	37777	8	SPBC215	AL033534 S.pombe c
14	1144.5	55.6	1288	8	D89184	D89184 Schizosacch
15	1082	52.6	135991	8	AP002882	AP002882 Oryza sat
16	1053.5	51.2	1209	6	AX489334	AX489334 Sequence

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 17:08:59 ; Search time 273 Seconds
                                     (without alignments)
                                     4063.989 Million cell updates/sec

Title: US-10-036-959B-8
Perfect score: 2057
Sequence: 1 MSPSSDSINPRDVCIVGVAR.........GASALVLELMSVGRVGRSLL 411

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US10036959/runat_04122003_161437_22942/app_query.fasta_1.5
83
-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10036959_@CGN_1_1_0_@runat_04122003_161437_22942 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_19Jun03:*
                 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                 4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                 5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                 6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                 7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                 8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                 9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                 10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*

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        11:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
        12:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
        13:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
        14:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
        15:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
        16:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
        17:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
        18:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
        19:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
        20:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
        21:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
        22:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
        23:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
        24:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
        25:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2057	100.0	1233	25	AAL55368	Acetyl-coA acetylt
2	1701	82.7	1418	21	AAC36444	Arabidopsis thalia
3	1701	82.7	1444	21	AAC40788	Arabidopsis thalia
4	1670	81.2	1212	21	AAA88448	Arabidopsis thalia
5	1670	81.2	1212	22	AAH27075	Arabidopsis thalia
6	1670	81.2	1510	21	AAC49943	Arabidopsis thalia
7	1668	81.1	1418	21	AAC49409	Arabidopsis thalia
8	1668	81.1	1446	21	AAC49408	Arabidopsis thalia
9	1665	80.9	1513	21	AAC36586	Arabidopsis thalia
10	1611	78.3	1650	21	AAC43767	Zea mays DNA fragm
11	1594.5	77.5	1606	21	AAC44677	Zea mays DNA fragm
12	1579.5	76.8	1462	22	AAD07039	Radish acetyl-CoA:
13	1579.5	76.8	1462	22	AAD03828	Raphanus sativus a
14	1122.5	54.6	1206	25	ABT20869	Aspergillus fumiga
15	1053.5	51.2	1209	24	ABZ32347	Candida albicans e
16	1031	50.1	1468	25	ABT20271	Aspergillus fumiga
17	1031	50.1	3468	25	ABT19675	Aspergillus fumiga
18	1026.5	49.9	1197	24	AAL40803	Nucleic acid relat
19	1026.5	49.9	1197	24	ABK96798	S. cerevisiae pren
20	1026.5	49.9	1197	24	AAD31016	Yeast acetoacetyl
21	1026.5	49.9	7681	24	AAD31026	Operon D DNA encod
22	1026.5	49.9	7693	24	AAD31023	Operon A DNA encod
23	1026.5	49.9	7695	24	AAD31024	Operon B DNA encod
24	1026.5	49.9	8077	24	AAD31028	Operon F DNA encod
25	1026.5	49.9	8224	24	AAD31027	Operon E DNA encod
26	1026.5	49.9	8235	24	AAD31025	Operon C encoding
27	1026.5	49.9	8400	24	AAD31029	Operon G DNA encod
28	1026.5	49.9	13917	24	AAD31037	Plastid transforma
29	1026.5	49.9	14623	24	AAD31039	Plastid transforma
30	1026.5	49.9	14623	24	AAD31041	Plastid transforma
c 31	1017	49.4	995	24	ABN98475	Arabidopsis thalia
32	948.5	46.1	1715	24	ABK63724	Rat sequence diffe

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 18:39:00 ; Search time 70 Seconds
                                              (without alignments)
                                              2591.550 Million cell updates/sec

Title: US-10-036-959B-8
Perfect score: 2057
Sequence: 1 MSPSSDSINPRDVCIVGVAR..........GASALVLELMSVGRVGRSLL 411

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US10036959/runat_04122003_161438_22982/app_query.fasta_1.5
83
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10036959_@CGN_1_1_44_@runat_04122003_161438_22982 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
                  1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                  2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                  3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                  4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                  5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                  6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1670	81.2	1212	4	US-09-503-391-7	Sequence 7, Appli
	2	1579.5	76.8	1462	4	US-09-672-749-12	Sequence 12, Appl
	3	884.5	43.0	1239	4	US-09-252-991A-3627	Sequence 3627, Ap
c	4	884.5	43.0	2034	4	US-09-252-991A-3835	Sequence 3835, Ap
	5	883.5	43.0	1182	4	US-09-252-991A-3677	Sequence 3677, Ap
c	6	861	41.9	1437	4	US-09-252-991A-14971	Sequence 14971, A
	7	861	41.9	1995	4	US-09-252-991A-14779	Sequence 14779, A
	8	857.5	41.7	1197	4	US-09-328-352-1131	Sequence 1131, Ap
	9	845	41.1	8625	3	US-08-980-832-1	Sequence 1, Appli
	10	845	41.1	11233	3	US-08-980-832-27	Sequence 27, Appl
	11	843	41.0	1221	4	US-09-328-352-3564	Sequence 3564, Ap
c	12	835.5	40.6	1830121	4	US-09-557-884-1	Sequence 1, Appli
c	13	835.5	40.6	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	14	831.5	40.4	1182	1	US-08-241-943-23	Sequence 23, Appl
	15	831.5	40.4	2327	6	5229279-5	Patent No. 5229279
	16	831.5	40.4	2327	6	5512669-5	Patent No. 5512669
	17	831.5	40.4	2328	4	US-09-672-749-11	Sequence 11, Appl
	18	831.5	40.4	4984	1	US-08-687-806-1	Sequence 1, Appli
	19	824	40.1	1254	4	US-09-252-991A-11478	Sequence 11478, A
	20	824	40.1	1524	4	US-09-252-991A-11455	Sequence 11455, A
c	21	824	40.1	2028	4	US-09-252-991A-11416	Sequence 11416, A
	22	822.5	40.0	1431	1	US-08-254-357-1	Sequence 1, Appli
	23	822.5	40.0	4983	1	US-08-472-358-1	Sequence 1, Appli
	24	822.5	40.0	4983	5	PCT-US92-05786A-1	Sequence 1, Appli
c	25	804.5	39.1	36470	4	US-08-311-731A-123	Sequence 123, App
	26	786	38.2	1200	4	US-09-134-001C-1730	Sequence 1730, Ap
	27	784.5	38.1	6977	4	US-08-178-257-8	Sequence 8, Appli
	28	780.5	37.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	29	780.5	37.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	30	723.5	35.2	2454	4	US-09-107-532A-755	Sequence 755, App
	31	695	33.8	1524	6	5512669-1	Patent No. 5512669
	32	691	33.6	1525	6	5229279-1	Patent No. 5229279
	33	648.5	31.5	1185	2	US-08-628-039-9	Sequence 9, Appli
	34	648.5	31.5	1185	3	US-08-912-205-9	Sequence 9, Appli
	35	648.5	31.5	1185	3	US-09-440-400-9	Sequence 9, Appli
	36	611.5	29.7	1230	4	US-09-328-352-3433	Sequence 3433, Ap
	37	608.5	29.6	1221	4	US-09-328-352-2438	Sequence 2438, Ap
	38	600.5	29.2	1224	4	US-09-328-352-3267	Sequence 3267, Ap
c	39	599	29.1	1992	4	US-09-252-991A-15580	Sequence 15580, A
	40	593	28.8	2208	4	US-09-252-991A-15669	Sequence 15669, A
	41	549.5	26.7	1275	4	US-09-252-991A-251	Sequence 251, App
c	42	549.5	26.7	1785	4	US-09-252-991A-281	Sequence 281, App
	43	548.5	26.7	1191	4	US-09-252-991A-2048	Sequence 2048, Ap
	44	548.5	26.7	1651	4	US-09-621-816B-7	Sequence 7, Appli
c	45	548.5	26.7	3546	4	US-09-252-991A-1909	Sequence 1909, Ap

ALIGNMENTS

RESULT 1
US-09-503-391-7

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 19:45:56 ; Search time 317 Seconds
                                         (without alignments)
                                         4309.146 Million cell updates/sec

Title: US-10-036-959B-8
Perfect score: 2057
Sequence: 1 MSPSSDSINPRDVCIVGVAR.........GASALVLELMSVGRVGRSLL 411

Scoring table: BLOSUM62
                   Xgapop 10.0 , Xgapext 0.5 ·
                   Ygapop 10.0 , Ygapext 0.5
                   Fgapop 6.0 , Fgapext 7.0
                   Delop   6.0 , Delext   7.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US10036959/runat_04122003_161439_23072/app_query.fasta_1.5
83
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10036959_@CGN_1_1_164_@runat_04122003_161439_23072
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA:*
                   1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                   2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                   3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                   4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                   5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                   6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                   7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                   8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                   9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                   10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

```
11:   /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12:   /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13:   /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14:   /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15:   /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16:   /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
17:   /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18:   /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2057	100.0	1233	15	US-10-036-959B-1	Sequence 1, Appli
	2	1690	82.2	1593	15	US-10-142-835-21	Sequence 21, Appl
	3	1630	79.2	2128	15	US-10-142-835-19	Sequence 19, Appl
	4	1602	77.9	1592	15	US-10-142-835-17	Sequence 17, Appl
	5	1122.5	54.6	1206	15	US-10-128-714-7219	Sequence 7219, Ap
	6	1053.5	51.2	1209	13	US-10-032-585-6634	Sequence 6634, Ap
	7	1031	50.1	1468	15	US-10-128-714-6219	Sequence 6219, Ap
	8	1031	50.1	3468	15	US-10-128-714-5219	Sequence 5219, Ap
	9	1026.5	49.9	1197	11	US-09-918-740-20	Sequence 20, Appl
	10	1026.5	49.9	1197	11	US-09-918-740-51	Sequence 51, Appl
	11	1026.5	49.9	1197	15	US-10-305-442-5	Sequence 5, Appli
	12	1026.5	49.9	7681	11	US-09-918-740-61	Sequence 61, Appl
	13	1026.5	49.9	7693	11	US-09-918-740-58	Sequence 58, Appl
	14	1026.5	49.9	7695	11	US-09-918-740-59	Sequence 59, Appl
	15	1026.5	49.9	8077	11	US-09-918-740-63	Sequence 63, Appl
	16	1026.5	49.9	8224	11	US-09-918-740-62	Sequence 62, Appl
	17	1026.5	49.9	8235	11	US-09-918-740-60	Sequence 60, Appl
	18	1026.5	49.9	8400	11	US-09-918-740-64	Sequence 64, Appl
	19	1026.5	49.9	13917	11	US-09-918-740-72	Sequence 72, Appl
	20	1026.5	49.9	14623	11	US-09-918-740-74	Sequence 74, Appl
	21	1026.5	49.9	14623	11	US-09-918-740-76	Sequence 76, Appl
c	22	1017	49.4	995	9	US-09-770-445-243	Sequence 243, App
	23	951	46.2	1227	15	US-10-305-442-3	Sequence 3, Appli
	24	948.5	46.1	1715	10	US-09-917-800A-1631	Sequence 1631, Ap
	25	944.5	45.9	696	15	US-10-036-959B-7	Sequence 7, Appli
	26	914.5	44.5	2405	10	US-09-981-353-156	Sequence 156, App
	27	845	41.1	8625	11	US-09-920-923-1	Sequence 1, Appli
	28	845	41.1	11233	11	US-09-920-923-27	Sequence 27, Appl
c	29	844.5	41.1	1911	15	US-10-305-442-1	Sequence 1, Appli
	30	844.5	41.1	1914	15	US-10-305-442-2	Sequence 2, Appli
	31	843	41.0	1176	13	US-10-166-225A-175	Sequence 175, App
	32	835.5	40.6	1182	9	US-09-815-242-6998	Sequence 6998, Ap
c	33	835.5	40.6	1830121	15	US-10-329-960-1	Sequence 1, Appli
	34	831.5	40.4	1182	10	US-09-364-847-1	Sequence 1, Appli
	35	831.5	40.4	1926	10	US-09-364-847-9	Sequence 9, Appli
	36	831.5	40.4	1926	10	US-09-364-847-18	Sequence 18, Appl
	37	822	40.0	1185	9	US-09-815-242-6183	Sequence 6183, Ap
	38	819	39.8	876	15	US-10-142-835-23	Sequence 23, Appl
	39	810.5	39.4	1182	9	US-09-815-242-7759	Sequence 7759, Ap

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 18:37:15 ; Search time 1951 Seconds
                                              (without alignments)
                                              5120.010 Million cell updates/sec

Title: US-10-036-959B-8
Perfect score: 2057
Sequence: 1 MSPSSDSINPRDVCIVGVAR.........GASALVLELMSVGRVGRSLL 411

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US10036959/runat_04122003_161438_22964/app_query.fasta_1.5
83
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10036959_@CGN_1_1_2135_@runat_04122003_161438_22964 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   EST:*
                 1: em_estba:*
                 2: em_esthum:*
                 3: em_estin:*
                 4: em_estmu:*
                 5: em_estov:*
                 6: em_estpl:*
                 7: em_estro:*
                 8: em_htc:*
                 9: gb_est1:*
                 10: gb_est2:*

```
            11:  gb_htc:*
            12:  gb_est3:*
            13:  gb_est4:*
            14:  gb_est5:*
            15:  em_estfun:*
            16:  em_estom:*
            17:  em_gss_hum:*
            18:  em_gss_inv:*
            19:  em_gss_pln:*
            20:  em_gss_vrt:*
            21:  em_gss_fun:*
            22:  em_gss_mam:*
            23:  em_gss_mus:*
            24:  em_gss_pro:*
            25:  em_gss_rod:*
            26:  em_gss_phg:*
            27:  em_gss_vrl:*
            28:  gb_gss1:*
            29:  gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1615	78.5	1749	11	AY103699	AY103699 Zea mays
2	1594.5	77.5	1879	11	AY105770	AY105770 Zea mays
3	1192	57.9	951	10	BG416085	BG416085 HVSMEk000
4	1159	56.3	843	14	CB975981	CB975981 CAB40001_
5	1064	51.7	867	14	CD575683	CD575683 UCRPT01_0
6	1061	51.6	910	10	BG415008	BG415008 HVSMEk000
7	1036	50.4	933	14	CD437615	CD437615 EL01N0503
8	1027	49.9	800	10	BG581423	BG581423 EST483156
9	1024.5	49.8	837	10	BF256599	BF256599 HVSMEf001
10	987.5	48.0	812	14	CB646206	CB646206 OSJNEb08I
11	974.5	47.4	699	9	AL750185	AL750185 AL750185
12	962	46.8	892	10	BG414978	BG414978 HVSMEk000
13	958.5	46.6	719	10	BG126595	BG126595 EST472241
14	955	46.4	851	14	CB671591	CB671591 OSJNEe05D
15	954	46.4	792	14	CB293333	CB293333 UCRCS01_0
16	950.5	46.2	741	10	BG597723	BG597723 EST496401
17	950.5	46.2	2526	11	AK032097	AK032097 Mus muscu
18	950.5	46.2	3374	11	AK081715	AK081715 Mus muscu
19	941	45.7	711	14	CA782432	CA782432 sat28g05.
20	940	45.7	682	14	CD479986	CD479986 eca01-30m
21	937.5	45.6	1566	11	BC024429	BC024429 Mus muscu
22	932	45.3	786	14	CB645964	CB645964 OSJNEb08B
23	927.5	45.1	674	13	BX250825	BX250825 BX250825
24	925	45.0	718	14	CB971300	CB971300 CAB10005_
25	923.5	44.9	662	10	BG450568	BG450568 NF036B09D
26	923.5	44.9	744	10	BG597276	BG597276 EST495954
27	922	44.8	872	10	BF258695	BF258695 HVSMEf001
28	921	44.8	682	10	BF634176	BF634176 NF074E12D

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2003, 12:16:12 ; Search time 3229 Seconds
                                         (without alignments)
                                         15621.421 Million cell updates/sec

Title: US-10-036-959B-1
Perfect score: 1233
Sequence: 1 atgtctccttcttcagattc..........gggtgggacgttcgttgtta 1233

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*

                 Seq ID NO: 1
                 in DNA databases
                 directly

                 1:   gb_ba:*
                 2:   gb_htg:*
                 3:   gb_in:*
                 4:   gb_om:*
                 5:   gb_ov:*
                 6:   gb_pat:*
                 7:   gb_ph:*
                 8:   gb_pl:*
                 9:   gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*

```
                28:   em_un:*
                29:   em_vi:*
                30:   em_htg_hum:*
                31:   em_htg_inv:*
                32:   em_htg_other:*
                33:   em_htg_mus:*
                34:   em_htg_pln:*
                35:   em_htg_rod:*
                36:   em_htg_mam:*
                37:   em_htg_vrt:*
                38:   em_sy:*
                39:   em_htgo_hum:*
                40:   em_htgo_mus:*
                41:   em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1233	100.0	1669	8	AF429383	AF429383 Hevea bra
	2	727.4	59.0	1444	8	AY088740	AY088740 Arabidops
	3	716.4	58.1	1736	8	AF364059	AF364059 Arabidops
	4	714.6	58.0	1492	8	AF411795	AF411795 Arabidops
	5	702	56.9	1228	8	AY091271	AY091271 Arabidops
	6	702	56.9	1531	8	AY059736	AY059736 Arabidops
	7	647	52.5	1462	6	AR242842	AR242842 Sequence
	8	647	52.5	1462	6	AX105331	AX105331 Sequence
	9	647	52.5	1462	6	AX105578	AX105578 Sequence
	10	647	52.5	1462	8	RSLAACT	X78116 R.sativus L
	11	433.6	35.2	960	8	AF429387	AF429387 Hevea bra
c	12	396.8	32.2	37777	8	SPBC215	AL033534 S.pombe c
	13	394.2	32.0	1288	8	D89184	D89184 Schizosacch
	14	389.8	31.6	1209	6	AX489334	AX489334 Sequence
c	15	383.4	31.1	256879	3	AC116982	AC116982 Dictyoste
	16	327.2	26.5	1707	8	YSACTPACTB	D13471 Candida tro
c	17	323.8	26.3	301150	1	AP004602	AP004602 Oceanobac
	18	322	26.1	971	8	AF113522	AF113522 Zea mays
	19	319.2	25.9	1702	8	YSACTPACTA	D13470 Candida tro
	20	314.2	25.5	1517	9	AB083303	AB083303 Macaca fa
	21	312.8	25.4	2277	8	YSCAACOAT	L20428 Saccharomyc
	22	312.8	25.4	27120	8	SCU36624	U36624 Saccharomyc
	23	312.6	25.4	1518	9	HUMMACT	D90228 Homo sapien
	24	312.2	25.3	1197	6	BD170977	BD170977 Process f
	25	312.2	25.3	1197	6	BD171096	BD171096 Process f
	26	311.2	25.2	300029	1	AE015936	AE015936 Clostridi
	27	303.2	24.6	1937	1	CAU08465	U08465 Clostridium
	28	303.2	24.6	2600	1	AF072734	AF072734 Clostridi
c	29	303.2	24.6	10907	1	AE007785	AE007785 Clostridi
	30	294.8	23.9	2001	8	SUERG10	X07976 Yeast (S. u
	31	293.4	23.8	1464	10	RATACAS	D13921 Rattus norv
	32	291.8	23.7	1715	6	AX401955	AX401955 Sequence
	33	291.8	23.7	1715	10	RATACAL	D00512 Rattus sp.

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2003, 12:16:07 ; Search time 299 Seconds
                                         (without alignments)
                                         11131.796 Million cell updates/sec

Title: .   US-10-036-959B-1
Perfect score: 1233
Sequence: 1 atgtctccttcttcagattc..........gggtgggacgttcgttgtta 1233

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_19Jun03:*
                  1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                  2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                  3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                  4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                  5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                  6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                  7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                  8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                  9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                  10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
                  11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
                  12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
                  13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
                  14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
                  15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
                  16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
                  17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
                  18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
                  19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
                  20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
                  21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
                  22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                  23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                  24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                  25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

       Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1233	100.0	1233	25	AAL55368	Acetyl-coA acetylt
	2	727.4	59.0	1418	21	AAC36444	Arabidopsis thalia
	3	727.4	59.0	1444	21	AAC40788	Arabidopsis thalia
	4	716.4	58.1	1212	21	AAA88448	Arabidopsis thalia
	5	716.4	58.1	1212	22	AAH27075	Arabidopsis thalia
	6	716.4	58.1	1510	21	AAC49943	Arabidopsis thalia
	7	714.8	58.0	1513	21	AAC36586	Arabidopsis thalia
	8	712	57.7	1418	21	AAC49409	Arabidopsis thalia
	9	712	57.7	1446	21	AAC49408	Arabidopsis thalia
	10	696.8	56.5	1650	21	AAC43767	Zea mays DNA fragm
	11	658	53.4	1606	21	AAC44677	Zea mays DNA fragm
	12	647	52.5	1462	22	AAD07039	Radish acetyl-CoA:
	13	647	52.5	1462	22	AAD03828	Raphanus sativus a
	14	433.6	35.2	696	25	AAL55374	Acetyl-coA acetylt
c	15	428	34.7	995	24	ABN98475	Arabidopsis thalia
	16	389.8	31.6	1209	24	ABZ32347	Candida albicans e
	17	365.8	29.7	1206	25	ABT20869	Aspergillus fumiga
	18	313.2	25.4	7681	24	AAD31026	Operon D DNA encod
	19	313.2	25.4	7693	24	AAD31023	Operon A DNA encod
	20	313.2	25.4	7695	24	AAD31024	Operon B DNA encod
	21	313.2	25.4	8077	24	AAD31028	Operon F DNA encod
	22	313.2	25.4	8224	24	AAD31027	Operon E DNA encod
	23	313.2	25.4	8235	24	AAD31025	Operon C encoding
	24	313.2	25.4	8400	24	AAD31029	Operon G DNA encod
	25	313.2	25.4	13917	24	AAD31037	Plastid transforma
	26	313.2	25.4	14623	24	AAD31039	Plastid transforma
	27	313.2	25.4	14623	24	AAD31041	Plastid transforma
	28	312.2	25.3	1197	24	AAL40803	Nucleic acid relat
	29	312.2	25.3	1197	24	ABK96798	S. cerevisiae pren
	30	312.2	25.3	1197	24	AAD31016	Yeast acetoacetyl
	31	291.8	23.7	1715	24	ABK63724	Rat sequence diffe
	32	267.4	21.7	567	22	AAH50938	Lipid degradation
	33	267.4	21.7	567	22	AAH56945	P patens lipid met
c	34	256.2	20.8	1830121	17	AAT42063	Haemophilus influe
	35	255.6	20.7	1468	25	ABT20271	Aspergillus fumiga
	36	255.6	20.7	3468	25	ABT19675	Aspergillus fumiga
	37	253.8	20.6	1182	23	AAS53361	Haemophilus influe
	38	251.2	20.4	1276	21	AAF13921	Aspergillus oryzae
	39	249	20.2	1200	24	ABN92267	Staphylococcus epi
	40	249	20.2	2988	22	AAH54768	S. epidermidis gen
c	41	249	20.2	3315	22	AAH54999	S. epidermidis gen
	42	241.6	19.6	11014	18	AAV74402	Staphylococcus aur
	43	239.6	19.4	1140	22	AAH53708	S. epidermidis ope
	44	238.2	19.3	483	21	AAC41012	Zea mays DNA fragm
	45	236.8	19.2	495269	24	ABQ67195	Listeria innocua c

ALIGNMENTS

```
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OM nucleic - nucleic search, using sw model

Run on:          December  8, 2003, 16:50:05 ; Search time 76 Seconds
                                         (without alignments)
                                         7160.861 Million cell updates/sec

Title:           US-10-036-959B-1
Perfect score:   1233
Sequence:        1 atgtctccttcttcagattc..........gggtgggacgttcgttgtta 1233

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters:      1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
                 1:  /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2:  /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3:  /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4:  /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5:  /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result              Query
   No.      Score  Match Length DB  ID                        Description
------------------------------------------------------------------------------
        1    716.4  58.1   1212   4  US-09-503-391-7          Sequence 7, Appli
        2    647    52.5   1462   4  US-09-672-749-12         Sequence 12, Appl
        3    291.6  23.6   1197   4  US-09-328-352-1131       Sequence 1131, Ap
        4    260.8  21.2   1221   4  US-09-328-352-3564       Sequence 3564, Ap
   c    5    256.2  20.8 1830121   4  US-09-557-884-1          Sequence 1, Appli
   c    6    256.2  20.8 1830121   4  US-09-643-990A-1         Sequence 1, Appli
        7    249    20.2   1200   4  US-09-134-001C-1730      Sequence 1730, Ap
        8    189.2  15.3   1239   4  US-09-252-991A-3627      Sequence 3627, Ap
   c    9    189.2  15.3   2034   4  US-09-252-991A-3835      Sequence 3835, Ap
       10    189    15.3   1182   4  US-09-252-991A-3677      Sequence 3677, Ap
       11    186.6  15.1   2454   4  US-09-107-532A-755       Sequence 755, App
```

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2003, 17:05:04 ; Search time 335 Seconds
                                        (without alignments)
                                        12232.829 Million cell updates/sec

Title: US-10-036-959B-1
Perfect score: 1233
Sequence: 1 atgtctccttcttcagattc..........gggtgggacgttcgttgtta 1233

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1:   /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                 2:   /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 3:   /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 4:   /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                 5:   /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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                 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
                 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

a glycine
man seg

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1233	100.0	1233	15	US-10-036-959B-1	Sequence 1, Appli
2	774.4	62.8	1593	15	US-10-142-835-21	Sequence 21, Appl
3	723.4	58.7	2128	15	US-10-142-835-19	Sequence 19, Appl
4	685	55.6	1592	15	US-10-142-835-17	Sequence 17, Appl
5	433.6	35.2	696	15	US-10-036-959B-7	Sequence 7, Appli
c 6	428	34.7	995	9	US-09-770-445-243	Sequence 243, App
7	389.8	31.6	1209	13	US-10-032-585-6634	Sequence 6634, Ap
8	365.8	29.7	1206	15	US-10-128-714-7219	Sequence 7219, Ap
9	353.6	28.7	876	15	US-10-142-835-23	Sequence 23, Appl
10	313.2	25.4	7681	11	US-09-918-740-61	Sequence 61, Appl
11	313.2	25.4	7693	11	US-09-918-740-58	Sequence 58, Appl
12	313.2	25.4	7695	11	US-09-918-740-59	Sequence 59, Appl
13	313.2	25.4	8077	11	US-09-918-740-63	Sequence 63, Appl
14	313.2	25.4	8224	11	US-09-918-740-62	Sequence 62, Appl
15	313.2	25.4	8235	11	US-09-918-740-60	Sequence 60, Appl
16	313.2	25.4	8400	11	US-09-918-740-64	Sequence 64, Appl
17	313.2	25.4	13917	11	US-09-918-740-72	Sequence 72, Appl
18	313.2	25.4	14623	11	US-09-918-740-74	Sequence 74, Appl
19	313.2	25.4	14623	11	US-09-918-740-76	Sequence 76, Appl
20	312.6	25.4	2405	10	US-09-981-353-156	Sequence 156, App
21	312.2	25.3	1197	11	US-09-918-740-20	Sequence 20, Appl
22	312.2	25.3	1197	11	US-09-918-740-51	Sequence 51, Appl
23	312.2	25.3	1197	15	US-10-305-442-5	Sequence 5, Appli
24	305.6	24.8	498	15	US-10-142-835-5	Sequence 5, Appli
25	291.8	23.7	1715	10	US-09-917-800A-1631	Sequence 1631, Ap
c 26	256.2	20.8	1830121	15	US-10-329-960-1	Sequence 1, Appli
27	255.6	20.7	1468	15	US-10-128-714-6219	Sequence 6219, Ap
28	255.6	20.7	3468	15	US-10-128-714-5219	Sequence 5219, Ap
29	253.8	20.6	1182	9	US-09-815-242-6998	Sequence 6998, Ap
30	246	20.0	1185	13	US-10-006-909-1	Sequence 1, Appli
31	246	20.0	4760	13	US-10-006-909-8	Sequence 8, Appli
32	246	20.0	9253	13	US-10-006-909-7	Sequence 7, Appli
33	241.6	19.6	11014	8	US-08-781-986A-91	Sequence 91, Appl
34	236.6	19.2	371	10	US-09-878-574-1702	Sequence 1702, Ap
35	234.4	19.0	1173	9	US-09-815-242-4541	Sequence 4541, Ap
36	234.4	19.0	1182	9	US-09-815-242-8319	Sequence 8319, Ap
c 37	233.2	18.9	505	11	US-09-770-961-311	Sequence 311, App
c 38	209.8	17.0	3249	9	US-09-925-301-457	Sequence 457, App
39	209.2	17.0	1185	9	US-09-815-242-6183	Sequence 6183, Ap
40	208.8	16.9	471	15	US-10-142-835-1	Sequence 1, Appli
41	206.2	16.7	1227	15	US-10-305-442-3	Sequence 3, Appli
42	206.2	16.7	1284	15	US-10-128-714-2219	Sequence 2219, Ap
43	202.4	16.4	1176	9	US-09-815-242-7259	Sequence 7259, Ap
44	194.4	15.8	1176	9	US-09-815-242-7428	Sequence 7428, Ap
45	188.4	15.3	2032	9	US-09-925-299-90	Sequence 90, Appl

ALIGNMENTS

RESULT 1
US-10-036-959B-1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2003, 16:34:14 ; Search time 2024 Seconds
                                             (without alignments)
                                             14806.037 Million cell updates/sec

Title: US-10-036-959B-1
Perfect score: 1233
Sequence: 1 atgtctccttcttcagattc..........gggtgggacgttcgttgtta 1233

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: em_estba:*
                 2: em_esthum:*
                 3: em_estin:*
                 4: em_estmu:*
                 5: em_estov:*
                 6: em_estpl:*
                 7: em_estro:*
                 8: em_htc:*
                 9: gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
                 19: em_gss_pln:*
                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
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                 26: em_gss_phg:*
                 27: em_gss_vrl:*

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        28:   gb_gss1:*
        29:   gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	696.4	56.5	1749	11	AY103699	AY103699 Zea mays
	2	658	53.4	1879	11	AY105770	AY105770 Zea mays
	3	545.8	44.3	843	14	CB975981	CB975981 CAB40001_
	4	541.4	43.9	951	10	BG416085	BG416085 HVSMEk000
	5	484	39.3	910	10	BG415008	BG415008 HVSMEk000
	6	482.8	39.2	867	14	CD575683	CD575683 UCRPT01_0
	7	447.6	36.3	933	14	CD437615	CD437615 EL01N0503
	8	446	36.2	719	10	BG126595	BG126595 EST472241
	9	443.2	35.9	792	14	CB293333	CB293333 UCRCS01_0
	10	436.8	35.4	682	14	CD479986	CD479986 eca01-30m
	11	436.6	35.4	706	13	BU866564	BU866564 S068C02 P
	12	434.2	35.2	800	10	BG581423	BG581423 EST483156
	13	433.6	35.2	711	14	CA782432	CA782432 sat28g05.
	14	433.4	35.2	714	14	CB975394	CB975394 CAB30007_
	15	430.2	34.9	892	10	BG414978	BG414978 HVSMEk000
	16	430	34.9	786	14	CB645964	CB645964 OSJNEb08B
	17	422.8	34.3	792	10	BG595837	BG595837 EST494515
	18	422.6	34.3	662	10	BG450568	BG450568 NF036B09D
	19	422.6	34.3	741	10	BG597723	BG597723 EST496401
	20	421.2	34.2	718	14	CB971300	CB971300 CAB10005_
	21	418.2	33.9	699	9	AL750185	AL750185 AL750185
	22	417.6	33.9	744	10	BG597276	BG597276 EST495954
	23	414.6	33.6	668	10	BG593575	BG593575 EST492253
	24	411.4	33.4	724	10	BG600757	BG600757 EST505652
	25	411.4	33.4	872	10	BF258695	BF258695 HVSMEf001
	26	407.6	33.1	688	10	BG593225	BG593225 EST491903
	27	405.4	32.9	674	13	BX250825	BX250825 BX250825
	28	405.2	32.9	664	13	BU862428	BU862428 S015E08 P
	29	404.8	32.8	733	13	BQ986779	BQ986779 QGF10G21.
	30	401.4	32.6	681	10	BG599647	BG599647 EST504542
	31	401.2	32.5	722	13	BX251062	BX251062 BX251062
c	32	400.6	32.5	703	14	CB978630	CB978630 CAB40006_
	33	399.6	32.4	682	10	BF634176	BF634176 NF074E12D
	34	399.6	32.4	688	12	BJ465084	BJ465084 BJ465084
c	35	399.4	32.4	648	14	CA926843	CA926843 MTU6CR.P1
	36	399	32.4	633	14	CB919089	CB919089 VVD041B12
	37	397.8	32.3	685	14	CB978562	CB978562 CAB40006_
c	38	397.2	32.2	650	14	CA926512	CA926512 MTU6CR.P1
	39	396.2	32.1	715	14	CB292001	CB292001 UCRCS01_0
	40	395.4	32.1	629	14	CB914934	CB914934 VVD098G02
c	41	395.2	32.1	648	14	CA927026	CA927026 MTU6CR.P4
	42	395	32.0	668	10	BE213442	BE213442 GF-FV-P6A
	43	394.2	32.0	784	10	BF275218	BF275218 GA__Eb002
	44	393	31.9	630	13	BU985298	BU985298 HF06L16r
	45	392	31.8	812	14	CB646206	CB646206 OSJNEb08I